

AMENDMENT TO THE SPECIFICATION

Please replace the paragraph beginning at page 3 line 28 with the following amended paragraph:

-- Search and identification of homologous nucleic acids, would be well within the realm of a person skilled in the art. Such methods[.]] involve screening sequence databases with the sequence provided by the present invention, for example any one of SEQ ID NO 1 to 22, preferably in a computer readable form. Useful sequence databases[.]] include but are not limited to Genbank (<http://www.ncbi.nlm.nih.gov/web/Genbank>), the European Molecular Biology Laboratory Nucleic acid Database (EMBL) (<http://www.ebi.ac.uk/ebi-docs/embl-db.html>) or versions thereof, or the MIPS database (<http://mips.gsf.de/>). Different search algorithms and software for the alignment and comparison of sequences are well known in the art. Such software includes, for example GAP, BSETFIT, BLAST, FASTA and TFASTA. Preferably BLAST software is used, which calculates percent sequence identity and performs a statistical analysis of the similarity between the sequences. The suite of programs referred to as BLAST programs has 5 different implementations: three designed for nucleotide sequence queries (BLASTN, BLASTX and TBLASTX) and two designed for protein sequence queries (BLASTP and TBLASTN) (Coulson, Trends in Biotechnology: 76-80, 1994; Birren et al., GenomeAnalysis, 1:543, 1997). The software for performing BLAST analysis is publicly available through the National Centre for Biotechnology information. --